

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/591,632C  
Source: IFW16  
Date Processed by STIC: 2/7/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>09/591,632C</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>    </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>    </u> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <u>    </u> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.	
4 <u>    </u> Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <u>    </u> Variable Length	Sequence(s) <u>        </u> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>    </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>        </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <u>    </u> Skipped Sequences (OLD RULES)	Sequence(s) <u>        </u> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <u>    </u> Skipped Sequences (NEW RULES)	Sequence(s) <u>        </u> missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>    </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of <b>n</b> or <b>Xaa</b> , and which residue <b>n</b> or <b>Xaa</b> represents.	
10 <u>   </u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 <u>   </u> Use of <220>	Sequence(s) <u>        </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>   </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>   </u> Misuse of n/Xaa	<b>"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid</b>	



IFW16

## RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

3 <110> APPLICANT: Lindquist, et al.  
 5 <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS AND  
 6 METHODS COMPRISING SAME  
 8 <130> FILE REFERENCE: 30554/34978A  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/591,632C  
 C--> 10 <141> CURRENT FILING DATE: 2000-06-09  
 10 <150> PRIOR APPLICATION NUMBER: US 09/591,632  
 11 <151> PRIOR FILING DATE: 2000-06-09  
 13 <150> PRIOR APPLICATION NUMBER: US 60/138,833  
 14 <151> PRIOR FILING DATE: 1999-06-09  
 16 <160> NUMBER OF SEQ ID NOS: 70  
 18 <170> SOFTWARE: PatentIn version 3.3

*Use of records  
 72 character*

*(see item 2 on*

*Error*

*summary*

*sheet)*

*delete -  
 there are  
 not prior  
 data. They  
 are current data.*

## ERRORED SEQUENCES

429 <210> SEQ ID NO: 3  
 430 <211> LENGTH: 1427  
 431 <212> TYPE: DNA  
 432 <213> ORGANISM: Saccharomyces cerevisiae  
 434 <220> FEATURE:  
 435 <221> NAME/KEY: CDS  
 436 <222> LOCATION: (182)..(1246)  
 438 <400> SEQUENCE: 3  
 439 ctcgagggttg aaaagaatag caaaaatctt tccttttcaa acagctcatt tggaattggt 60  
 441 tatagcactg aattgaatcg aagaggaata aagatccccc gtacgaactt ctttattttt 120  
 443 agtttttcat tttttgttat tagtcatatt gttttaagct gcaaattaag ttgtacacca 180  
 445 a atg atg aat aac aac ggc aac caa gtg tcg aat ctc tcc aat gcg ctc 229  
 446 Met Met Asn Asn Asn Gly Asn Gln Val Ser Asn Leu Ser Asn Ala Leu  
 447 1 5 10 15  
 449 cgt caa gta aac ata gga aac agg aac agt aat aca acc acc gat caa 277  
 450 Arg Gln Val Asn Ile Gly Asn Arg Asn Ser Asn Thr Thr Thr Asp Gln  
 451 20 25 30  
 453 agt aat ata aat ttt gaa ttt tca aca ggt gta aat aat aat aat aat 325  
 454 Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn  
 455 35 40 45  
 457 aac aat agc agt agt aat aac aat aat gtt caa aac aat aac agc ggc 373  
 458 Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly  
 459 50 55 60  
 461 cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc 421  
 462 Arg Asn Gly Ser Gln Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr  
 463 65 70 75 80  
 465 tta gaa caa cat cga caa caa caa cag gca ttt tcg gat atg agt cac 469

**Does Not Comply  
 Corrected Diskette Needed**

*pp 1, 3, 5-6, 7*

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Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

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467					85					90					95		
469	gtg	gag	tat	tcc	aga	att	aca	aaa	ttt	ttt	caa	gaa	caa	cca	ctg	gag	517
470	Val	Glu	Tyr	Ser	Arg	Ile	Thr	Lys	Phe	Phe	Gln	Glu	Gln	Pro	Leu	Glu	
471				100					105					110			
473	gga	tat	acc	ctt	ttc	tct	cac	agg	tct	gcg	cct	aat	gga	ttc	aaa	gtt	565
474	Gly	Tyr	Thr	Leu	Phe	Ser	His	Arg	Ser	Ala	Pro	Asn	Gly	Phe	Lys	Val	
475			115					120					125				
477	gct	ata	gta	cta	agt	gaa	ctt	gga	ttt	cat	tat	aac	aca	atc	ttc	cta	613
478	Ala	Ile	Val	Leu	Ser	Glu	Leu	Gly	Phe	His	Tyr	Asn	Thr	Ile	Phe	Leu	
479		130					135					140					
481	gat	ttc	aat	ctt	ggc	gaa	cat	agg	gcc	ccc	gaa	ttt	gtg	tct	gtg	aac	661
482	Asp	Phe	Asn	Leu	Gly	Glu	His	Arg	Ala	Pro	Glu	Phe	Val	Ser	Val	Asn	
483	145				150					155					160		
485	cct	aat	gca	aga	gtt	cca	gct	tta	atc	gat	cat	ggg	atg	gac	aac	ttg	709
486	Pro	Asn	Ala	Arg	Val	Pro	Ala	Leu	Ile	Asp	His	Gly	Met	Asp	Asn	Leu	
487				165					170					175			
489	tct	att	tgg	gaa	tca	ggg	gcg	att	tta	tta	cat	ttg	gta	aat	aaa	tat	757
490	Ser	Ile	Trp	Glu	Ser	Gly	Ala	Ile	Leu	Leu	His	Leu	Val	Asn	Lys	Tyr	
491			180					185					190				
493	tac	aaa	gag	act	ggg	aat	cca	tta	ctc	tgg	tcc	gat	gat	tta	gct	gac	805
494	Tyr	Lys	Glu	Thr	Gly	Asn	Pro	Leu	Leu	Trp	Ser	Asp	Asp	Leu	Ala	Asp	
495			195				200					205					
497	caa	tca	caa	atc	aac	gca	tgg	ttg	ttc	ttc	caa	acg	tca	ggg	cat	gcg	853
498	Gln	Ser	Gln	Ile	Asn	Ala	Trp	Leu	Phe	Phe	Gln	Thr	Ser	Gly	His	Ala	
499		210				215					220						
501	cca	atg	att	gga	caa	gct	tta	cat	ttc	aga	tac	ttc	cat	tca	caa	aag	901
502	Pro	Met	Ile	Gly	Gln	Ala	Leu	His	Phe	Arg	Tyr	Phe	His	Ser	Gln	Lys	
503	225				230					235					240		
505	ata	gca	agt	gct	gta	gaa	aga	tat	acg	gat	gag	gtt	aga	aga	gtt	tac	949
506	Ile	Ala	Ser	Ala	Val	Glu	Arg	Tyr	Thr	Asp	Glu	Val	Arg	Arg	Val	Tyr	
507			245					250					255				
509	ggg	gta	gtg	gag	atg	gcc	ttg	gct	gaa	cgt	aga	gaa	gcg	ctg	gtg	atg	997
510	Gly	Val	Val	Glu	Met	Ala	Leu	Ala	Glu	Arg	Arg	Glu	Ala	Leu	Val	Met	
511			260					265					270				
513	gaa	tta	gac	acg	gaa	aat	gcg	gct	gca	tac	tca	gct	ggg	aca	aca	cca	1045
514	Glu	Leu	Asp	Thr	Glu	Asn	Ala	Ala	Ala	Tyr	Ser	Ala	Gly	Thr	Thr	Pro	
515			275				280						285				
517	atg	tca	caa	agt	cgt	ttc	ttt	gat	tat	ccc	gta	tgg	ctt	gta	gga	gat	1093
518	Met	Ser	Gln	Ser	Arg	Phe	Phe	Asp	Tyr	Pro	Val	Trp	Leu	Val	Gly	Asp	
519		290				295					300						
521	aaa	tta	act	ata	gca	gat	ttg	gcc	ttt	gtc	cca	tgg	aat	aat	gtc	gtg	1141
522	Lys	Leu	Thr	Ile	Ala	Asp	Leu	Ala	Phe	Val	Pro	Trp	Asn	Asn	Val	Val	
523	305				310					315					320		
525	gat	aga	att	ggc	att	aat	atc	aaa	att	gaa	ttt	cca	gaa	gtt	tac	aaa	1189
526	Asp	Arg	Ile	Gly	Ile	Asn	Ile	Lys	Ile	Glu	Phe	Pro	Glu	Val	Tyr	Lys	
527			325						330					335			
529	tgg	acg	aag	cat	atg	atg	aga	aga	ccc	gcg	gtc	atc	aag	gca	ttg	cgt	1237
530	Trp	Thr	Lys	His	Met	Met	Arg	Arg	Pro	Ala	Val	Ile	Lys	Ala	Leu	Arg	

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Input Set : A:\34978a.txt

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531          340          345          350
533 ggt gga tga aggtctgttt aaaaacaaga aagaaagaag aaggaggaaa      1286
534 Gly Gly
537 agaaggttat aagggtatgt atataggcag acaaaaagga aaattaagtg caaatataaa      1346
539 caaaaatgtc atagaagtat ataatagttt tgaaatttct gttgcttcta tttattcttt      1406
E--> 541 gttaccccaa ccacagaatt      1427/1426
724 <210> SEQ ID NO: 11
725 <211> LENGTH: 446 445
726 <212> TYPE: DNA
727 <213> ORGANISM: Artificial sequence
729 <220> FEATURE:
730 <223> OTHER INFORMATION: CUP1 promoter
732 <400> SEQUENCE: 11
733 ccattaccga catttggcgc ctatacgtgc atatgttcat gtatgtatct gtatttaaaa      60
735 cacttttcta ttatttttcc tcatatatgt gtataggttt atacggatga tttaattatt      120
737 acttcaccac cctttatttc aggtctgatat cttagccttg ttactagtta gaaaaagaca      180
739 tttttgctgt cagtcactgt caagagattc ttttgctggc atttcttcta gaagcaaaaa      240
741 gagcgatgcg tcttttccgc tgaaccgttc cagcaaaaaa gactaccaac gcaatatgga      300
743 ttgtcagaat catataaaaag aagaagcaaa taactccttg tcttgatca attgcattat      360
745 atatcttctt gttagtcaa tatcatatag aagtcacga aatagatatt aagaaaaaca      420
E--> 747 aactgtacaa tcaatcaatc aatca      445
3712 <210> SEQ ID NO: 45
3713 <211> LENGTH: 7239 7238 (p 5-6)
3714 <212> TYPE: DNA
3715 <213> ORGANISM: Artificial sequence
3717 <220> FEATURE:
3718 <223> OTHER INFORMATION: Vector containing chimeric gene
3720 <400> SEQUENCE: 45
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3725 atttgggaat ttactctgtg tttatttatt tttatgtttt gtatttggat tttagaaagt      180
3727 aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa aataaacaac ggtttaaaaa      240
3729 atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata      300
3731 gatatacatt cgattaacga taagtaaaat gtaaaatcac aggattttcg tgtgtggtct      360
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3735 aaaggtagta tttgttggcg atccccctag agtcttttac atcttcggaa aacaaaaaact      480
3737 attttttctt taatttcttt ttttactttc tatttttaat ttatatattt atattaaaaa      540
3739 atttaaatta taattatttt tatagcacgt gatgaaaagg acccaggtgg cacttttcgg      600
3741 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg      660
3743 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt      720
3745 attcaacatt tccgtgtcgc ccttattccc tttttgcgg cattttgcct tccgtttttt      780
3747 gctcaccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg      840
3749 ggttacatcg aactggatct caacagcggg aagatccttg agagttttcg ccccgagaa      900
3751 cgttttccaa tgatgagcac ttttaaagt tctgctatgt gcgcggtatt atcccgatt      960
3753 gacgcggggc aagagcaact cggtcgcccgc atacactatt ctcaaatga cttggttgag      1020
3755 tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt      1080
3757 gctgccataa ccatgagtga taacactgcg gccaaacttac ttctgacaac gatcggagga      1140
3759 ccgaaggagc taaccgcttt tttgcacaac atgggggatc atgtaactcg ccttgatcgt      1200
3761 tgggaaccgg agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta      1260

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Input Set : A:\34978a.txt

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3769	atcattgcag	cactggggcc	agatggtaag	ccctcccgtg	tcgtagttag	ctacacgacg	1500
3771	gggagtcagg	caactatgga	tgaacgaaat	agacagatcg	ctgagatagg	tgccctcactg	1560
3773	attaagcatt	ggtaactgtc	agaccaagtt	tactcatata	tacttttagat	tgatttaaaa	1620
3775	cttcattttt	aatttaaaag	gatctagggtg	aagatccttt	ttgataatct	catgaccaaa	1680
3777	atcccctaac	gtgagttttc	gttccactga	gcgtcagacc	ccgtagaaaa	gatcaaagga	1740
3779	tcttcttgag	atcctttttt	tctgcgcgta	atctgctgct	tgcaaacaaa	aaaaccaccg	1800
3781	ctaccagcgg	tggtttggtt	gccggatcaa	gagctaccaa	ctctttttcc	gaaggtaact	1860
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3785	cacttcaaga	actctgtagc	accgcctaca	tacctcgctc	tgctaactct	gttaccagtg	1980
3787	gctgctgcc	gtggcgataa	gtcgtgtcct	accgggttgg	actcaagacg	atagttaccg	2040
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3793	gaagggagaa	aggcggacag	gtatccggta	agcggcaggg	tcggaacagg	agagcgcacg	2220
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3813	aaccctcact	aaagggaaac	aaagctgggt	accgggcccc	ccctcgaggt	cgacgggtatc	2820
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3839	taagggttct	tcccaaacgc	aactaggaaa	actagctttg	ttagccacag	tgatgacaca	3600
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3845	tcaattcttt	aagtgcagga	acaattccca	aggtcagggg	caaggtcaag	gtcaaggtca	3780
3847	aggtcaagga	caaggtcaag	gtcaaggttc	ttttactgct	ttggcgtctt	tggttctatc	3840
3849	tttcatgaat	tccaacaaca	ataatcagca	aggtcaaaat	caaagctccg	gtggttcttc	3900
3851	ctttggagca	ctagcttcta	tggcaagttc	tttatgtcat	tccaataata	atcagaactc	3960
3853	caacaatagt	caacagggtt	ataaccaatc	ctatcaaaac	ggtaaccaaa	atagtcagg	4020
3855	ttacaataat	caacagtacc	aagggtggcaa	cggtgggttac	caacaacaac	agggacaatc	4080
3857	tggtgggtgct	ttttcctcat	tggcctccat	ggctcaatct	tacttaggtg	gtggacaaac	4140
3859	tcaatccaac	caacagcaat	acaatcaaca	aggccaaaac	aaccagcagc	aataccagca	4200

## RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

group  
9  
↑

```

3861 acaaggccaa aactatcagc accaacaaca gggtcagcag cagcaacaag gccactccag 4260
3863 ttcattctca gctttggctt ccatggcaag ttcctacctg ggcaataact ccaattcaaa 4320
3865 ttcgagttat gggggccagc aacaggctaa tgagtatggt agaccacaac acaatgggtca 4380
3867 acaacaatct aatgagtacg gaagaccgca atacggcgga aaccagaact ccaatggaca 4440
E--> 3869 gcacgaatcc cttaattttt ctggcaactt ttctcaacag aacaataacg gcaaccagaa 4500
E--> 3871 ccgctaccgg cggatggcta gcaaaggaga agaactcttc actggagttg tcccaattct 4560
E--> 3873 tgttgaatta gatggtgatg ttaatgggca caaattttct gtcagtggag aggggtgaagg 4620
E--> 3875 tgatgcaaca tacggaaaac ttacccttaa atttatttgc actactggaa aactacctgt 4680
E--> 3877 tccatggcca acacttgtca ctactttcac ttatggtggt cagtgtcttt caagataccc 4740
E--> 3879 ggatcatatg aaacggcatg actttttcaa gagtgccatg cccgaagggt atgtacagga 4800
E--> 3881 aagaactata tttttcaaag atgacgggaa ctacaagaca cgtgctgaag tcaagtttga 4860
E--> 3883 aggtgatacc cttgttaata gaatcgagtt aaaaggtatt gattttaaag aagatggaaa 4920
E--> 3885 cattcttggg cacaaaatgg aatacaacta taactcacac aatgtataca tcatggcaga 4980
E--> 3887 caaacaaaag aatggaatca aagctaaact caaaattaga cacaacattg aagatggaa 5040
E--> 3889 cgttcaacta gcagaccatt atcaacaaaa tactccaatt ggcatggcc ctgtcctttt 5100
E--> 3891 accagacaac cattacctgt ccacacaatc tgccctttcg aaagatccca acgaaaagag 5160
E--> 3893 agaccacatg gtcttctctg agtttgtaac agctgctggg attacacatg gcatggatga 5220
E--> 3895 actatacaaa tgagagctcc aattcgccct atagtgaatc gtattacaat tcactggccg 5280
E--> 3897 tcgtttttaca acgtcgtgac tgggaaaacc ctggcgctac ccaacttaat cgccttgacg 5340
E--> 3899 cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgccttccc 5400
E--> 3901 aacagttgag cagcctgaat ggcgaaatggc gcgacgcgcc ctgtagcggc gcattaagcg 5460
E--> 3903 cggcgggtgt ggtggttacg cgcagcgtga ccgctacact tgccagcgcc ctacgcgccg 5520
E--> 3905 ctcttttcgc tttcttccct tcctttctcg ccacgttcgc cggctttccc cgtcaagctc 5580
E--> 3907 taaatcgggg gctcccttta gggttccgat ttagtgcttt acggcacctc gaccccaaaa 5640
E--> 3909 aacttgatta gggatgatgt tcacgtatgt ggccatcgcc ctgatagacg gtttttcgcc 5700
E--> 3911 ctttgacgtt ggagtcacag ttctttaata gtggactctt gttccaaact ggaacaacac 5760
E--> 3913 tcaaccctat ctcggtctat tcttttgatt tataagggat tttgccgatt tcggcctatt 5820
E--> 3915 ggtaaaaaaa tgagctgatt taacaaaaat ttaacgcgaa ttttaacaaa atattaacgt 5880
E--> 3917 ttacaatttc ctgatgcggt attttctcct tacgcaatct tgcgggtatt cacaccgat 5940
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E--> 3921 ttacttataa tacagttttt tagttttgct ggccgcatct tctcaaatat gcttcccagc 6060
E--> 3923 ctgcttttct gtaacgttca cctctacact tagcatccct tccctttgca aatagtcctc 6120
E--> 3925 ttccaacaat aataatgtca gatcctgtag agaccacatc atccacgggt ctatactgtt 6180
E--> 3927 gacccaatgc gtctcccttg tcatctaaac ccacaccggg tgtcataatc aaccaatcgt 6240
E--> 3929 aaccttcac tcttccaccc atgtctcttt gagcaataaa gccgataaca aaatctttgt 6300
E--> 3931 cgtctcttcg aatgtcaaca gtacccttag tatattctcc agtagatagg gagcccttgc 6360
E--> 3933 atgacaattc tgctaacatc aaaaggcctc taggttcctt tgttacttct tctgccgcct 6420
E--> 3935 gcttcaaacc gctaacaata cctgggcca ccacaccgtg tgcattcgta atgtctgcc 6480
E--> 3937 attctgctat tctgtataca ccgcagagt actgcaattt gactgtatta ccaatgtcag 6540
E--> 3939 caaattttct gtcttcgaag agtaaaaaat tgtacttggc ggataatgcc tttagcgggt 6600
E--> 3941 taactgtgcc ctccatggaa aaatcagtca agatatccac atgtgttttt agtaaacaaa 6660
E--> 3943 ttttgggacc taatgcttca actaactcca gtaattcctt ggtggtacga acatccaatg 6720
E--> 3945 aagcacacaa gtttgtttgc ttttcgtgca tgatattaaa tagcttgga gcaacaggac 6780
E--> 3947 taggatgagt agcagcacgt tccttatatg tagctttcga catgatttat ctctgcttcc 6840
E--> 3949 tgcaggtttt tgttctgtgc agttgggtta agaatactgg gcaatttcac gtttcttcaa 6900
E--> 3951 cactacatat gcgtatatat accaaatctaa gtctgtgctc ctctctctgt tcttcttct 6960
E--> 3953 gttcggagat taccgaatca aaaaaatttc aaagaaaccg aaatcaaaaa aaagaataaa 7020
E--> 3955 aaaaaaatga tgaattgaat tgaaaagctg tggatgggtg cactctcagt acaatctgct 7080
E--> 3957 ctgatgccgc atagttaagc cagccccgac acccgccaac acccgctgac gcgccctgac 7140

```

4500 4499

number  
ff

## RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

E--> 3959 gggcttgtct gctccccggca tccgcttaca gacaagctgt gaccgtctcc gggagctgca  
E--> 3961 tgtgtcagag gttttcaccg tcatcaccga aacgcgcga

7200  
7239

hos.  
off



from sequence 39

09/591,632C

7

gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga 720  
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp glu Leu Tyr Lys  
225 230 235

(240) delete, since  
no amino  
acid  
is shown

VERIFICATION SUMMARY

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:24

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:541 M:254 E: No. of Bases conflict, LENGTH:Input:1427 Counted:1426 SEQ:3 ✓  
L:541 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1427 Found:1426 SEQ:3 ✓  
L:747 M:252 E: No. of Seq. differs, <211> LENGTH:Input:446 Found:445 SEQ:11 ✓  
L:3593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39 ✓  
L:3869 M:254 E: No. of Bases conflict, LENGTH:Input:4500 Counted:4499 SEQ:45 ✓  
M:254 Repeated in SeqNo=45  
L:3961 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7239 Found:7238 SEQ:45 ✓